

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTGACGAGCCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTGAGTAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCAGCCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCCCAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTCTGC
ATTCACCCACTGGCCTTTCCCACTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTGTCT
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTCTCGGCCACTGGTGAATCTGAGGGGTGA
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TGCAAATAAATGCAGATGATTGCGCGCTTTGAAAAAAAAA

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVS
SRKQQNVQDAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFPG
SIMDVTEEVWDKTLDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEEESMKETLRIRRLGEPEDC
AGIVSFLCEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCGGCGGCG
 CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGACCCCTGCAGAACAGAGTGCG
 CGCGCTGGAGGAGGAGAACCGGAGACTTCTGCTGCGCTGGAGGACGCCATGAGGAGCAGTACAACTGC
 AGAGCGACCGGCTGCGTGAAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGCGG
 CCAGGCTGGGGGGGCTGCGGCTCTGAATGGCTGCGCTCCGGGTCTTTGTGCTGCACCTATAC
 AGCCCCCTGGGGGGTGGCCACGCCCATGTGTGGGCATGGTGCCGCTGCGCTGCCCTCCCTGGAGATG
 AAGTTGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGAGGCTGGAGCTGAGTTGTGCTGACT
 GAGGTGAACAGGCTGGGAAGTGGCTCTTCACTGCTTCAAGGAGGAAGAGGAGGAGGAGGAGGCCGC
 CAGGCGGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCAG
 GGAGTCTGCCAGAGAGGAAGGGGCCAGAGCTTGTGCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
 AGAGCAGTTGGTGGGAGCAGGCCGAGTTCAGGCCCGCAGGTCCCCCTGCCACAGCCTCAGAGTG
 GCGGCTGGCCAGGCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
 TTGGCAGCTGGTCCGCAGGAAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG
 GAGCTGGAGCAGGAGGCAGAGCGGTGCGGCCGAGCTGAGTGAAGGCCAGGAGCAGCTGCGGGAGCT
 CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGAGGAGGGTGCCTG
 CGGCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTCTACTGCTCG
 GCCCAGAGTGAGGAAGCACTGCAGGAGCTCGAGCGGAAGTGCAGCTCATGCGGCAGCAGCAGGAGCA
 GCTCGCAGAGCGGCTTCCGAGGAGACGGAGCAGAAGCGGCGCTGGAGGACAGAAATGAGCAAGCGGC
 AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGTCTGAAGATTAAGACGGAA
 GAGATCGCGGCTTCCAGAGAGGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAAGCTGGAACAGCA
 GCAGAAATTGAGGAGCAGAAAGTGGCTGGACAGGAGATGGAGAAGTGCTACAGCAGCGGCGGG
 CGCTGGAGGAGCTGGGGAGGAGCTCCACAGCGGGAGGCCATCTGGCGCAAGAGGAGGCCCTGATG
 CAGGAGAAGACGGGGCTGGAGAGCAAGCGCTGAGATCCAGCCAGGCCCTCAACAGGAGACATCTGCG
 AGTGTCCAGCCGGCTGGAGCACTGGAGAAGGAGCTGTCCGAGAAGAGCGGCAGCTGCGGCAGGGCA
 GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC
 AAGCAGCGCTCGGAGATCGACGCGAAGCTGAGGCAGGGGAGTCTGCTGTCCCCCGAGGAGGAGCGGAC
 GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAAGATGAGGCCATCA
 CATGCCGCCAGCGGGTGCTCGGGCTCAGCCTCGTTGCTGTGCCAGTGCGAGATGAACCTCAGTGGCC
 AAGCTCAGCTACCTCTCATCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTGACAGAGTGTTGAC
 GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCGCTTCCGAACTGGAGATCGAGCTGGAGAGGAGCAGC
 AGAGGCTGGTGTACTGGCTGGAGTGCGCTCGAGCGGAGCGCTGGAGATGGACCAGCTGACC
 CTGCAAGCAGAAGGAGCAGCAGCAGAACATGCAGCTGCTCCTGCAAGAGTGGAGACCACCTCGGTGA
 AGGGITAGCAGACAGCAGGAGGAGATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACTGGGCCGTT
 ACATGTGGATAAACCCAGGAAGTGAACAGAAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
 GGGGAGAAGAGGAGCTGTGCTCGGAGGGCAGACAGGCTCCTGGAATGAAGATGAGCTCCACCTGGC
 ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACCGGGAGCT
 TGGTCCACGCTCCGTTACCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGGAGGAGCAGGGGTCCCC
 GAGGAACCTGAGGAGCGGGAGGGCGCTGAGCCCTGGTGGGGCGGGTGTCTCTCTGGTGGTGAGGAGC
 CTGCGCTGTACCTTTGGGCTTTGTCCAAAGCCCCGGCGGAACCTGCAGCAGCCAGCCCGGGGATGA
 TTGATGTCCGAAAAACCCCTGTAAAGCCCTCGGGGAGAGCCCTGCTGGAGGGAGACTCGAGCCT
 GCTGAAAGGGGAGCTGCTGTTTGTCTTGTGAAGGCGAGTCTTACCGCACCCCTAAATCAAGC
 CCTCATCTGTACCTCTGCTGGATCAACAAATTTGGGCCATGGCCCAAAGAACTGGACCCCTATTT
 AACAAATAATATGCAAAATCCACCACTTACTTCCATGAAGCTGTGGTACCAATTTGCCGCTGTG
 TCTTGCTCAATCTCAGACAAATCTGGTTTCAGCGTAATAGTGTGCTGTGATGTCAGGGGTTTG
 GCCAAGATCATCAGAAAGGGTCGGTGGCAACCAGGTGTGGTTTAAATGGTCTTATGTATATAGG
 GAAACTGGGAGACTTAGGATCTTAAAAAAACATTTAATAAAAAAAATCTTTGAGGGAGC

1033357-122701

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKQLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLNGLPPGSFVPRPHTAPLGGAAHVV
LGMVPPACLPGEVGVSEQRGEQVNTGREAGAELLTEVNRLGSGSSAAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPELCEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQGQLQRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQKRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQRRRALEELGELHKKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSASQQQIRGEIDS
LRQEKDSLKQRLRIDGKLRQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSESSETRALLCKYFDKVVTLREEQHQQQIAFSELEMQLEEQR
LVYWLEVALERQRLLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEQRIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPELLWLWSPLTEG
APRTREETRDVLVHAPLPLTWKRSSLGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCCTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCCGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCATTAAAACCCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACCTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCTTTCCAGCTCCCCTTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCACATTTACCATCT

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS

LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPIRSCTRNRHVLYP

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

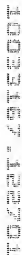


FIGURE 7

CCCACGCGTCCGCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
TTTCCCTCCGACGCGCCACGGCTGCCAGACATTCGGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGCTCTCG
GAGAAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
GGGGCCGCGACTACCGGCGAGTACAGCGCGATGAGCGACTCCCGAGAGCGCCCTAGCCCG
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTAGTGGTCCGCCCCACGCGGG
TCGCGGGCCGGCCAGGATGGGCGCTGGCAACCCGGGCGCGCGCCCGCTGCTACCCCTG
CGCCCGCTGCGAGCCCGCGTCCGGCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG
GCGGCGGCGCGCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCGCC
GCCCGCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCTGGTCACTGCTGCTGATGGTGGTCTGTGCGAGTCCGAGCATCCCGCTGGAG
AAGCTGGCCAGGCACCGAGCAGCCGGGCCAGGAGAAGCGTGAGCAGCCACTCGGGACGG
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGCGAGGGACGAGGGCGGCGGGCCGGGACT
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCAGGGCGGGGGCGCCAAGGCCGGGATCTGCAAGTCCGGCCCCCGGGGACAC
CCCGCAGGCGGAAGCCCTGGCCGCGAGCCGCCAGGACGCGATTGGCCCCGAACTCGCGCCCA
CGCCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCTCGGCTGCCCCGTCCT
GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGTGC
TCCACGTGCACACGAGCCAGTGTGCCCCGAGTGCAAGGAGAGGAAGAATACTGCGAGTT
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCAGACGGAGTGTGTGGACC
CTGTGTACGAGCCTGATCAGTGTGTCCCATCTGCAAAAATGGTCCAACTGCTTTGCAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATGTAGACGCTTCCCGAACAACAACTCTGACTTTTCTAGAACATTTTACTGATGTGAA
CATTTAGATGACTCTGGGAACATCAGTCAAAGAAGACTTTTGATGAGGAATAATGAAAAA
TTGTTGGTACTTTTCTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTT
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACG
TAAGTACACAAAGTACACTATTATATCAAAATGTATTTCTATAATCCCTCCATTAGAGAG
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTGTCAACCGTCAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 8

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSSLLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL
GRPARDEGGSGRDWKSksgrGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTTPQAEALA
AAQDAIGPELAPTPEPPPEEYVYPDYRGKGCVDSESGFVYAIGKEKFAPGPSACPCLTCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCRRCRCEANGEVL
CTVSACPQTECVDPVYEPDQCCPIKNGPNCFAETAIVIPAGREVKTDTECTICHCTYEETWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGTGTCTGTCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCTCAAGGGTGACACGG
AGGCCAAGGACAGGAGCCCCGCGTCACTGAGCACCGGATGGGGCCCCGGCCTCTCCTGATC
TCCTACACCTTCGTGTGTCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGATGCATGCC
CCAGCCAGGTTGCAACTGTCTCAATGGGACACAGGAAATGGGCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAAGATTTTCTGACCTGTATCGGGGACCACCATATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCAGATGTGCGAGGTGGGGCAGGT
GTGTGAGGAGACGCTGTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAACACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTAGGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGACGCCTCCTGCCTCTCAGCATGAGGAGGT
GGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGCCTTCTGCTTAACTCTATTACCCCCAGATTCTTACCCTGCTGTA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACAATCATTCATATCTACTCACCTAACAGCA
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GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

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><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
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ESGPQVSVLVLKSGCTEAKDQEPRVTEHRMGPGLSLSYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTCGSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQLGTCSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLNHNTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVCPSC
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG
GCTGCGGCGCTGCTCTCGTTCGCTTGCAGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGC
CTCGTTCGCTCAGCCCTATTTTCGGCACCAAGACTCGTACGAGGATGTCAACCCCGTGTCTAT
TGTCCGGCCCCGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGCTGGTTCGCCCTCATTTCGCCACGGCACCCGCTACCCACCGTCAAACAGATCCGCAAGCT
GAGGCGCGACCTGGGTTCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC
GGGAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCGCTGCCGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCGCCTTCTGTCAGGGGCTGTGGCAGCACTACCACCCGTGGC
TTGCCCGCGCCGGACGTCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTTGTACTGTCGAGAAGTTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT
ATCACGTGGGAAGCTTCAAACTGGACCAAGATGCAGAACATTTTAAAAAAAGTTGCAGCT
ACTTTCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTCACCTG
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CGGTACAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATGTACCTTATGC
CTCGAACCTGATATTTGTGCTTTACCAGTGTGAAATGTCTAAGACTCCTAAAGAACAAATTC
GAGTGCAGATGTTTATTAATGAAAAGGTGTACCTTTGGCTTACTCACAAGAACTGTTTCA
TTTTATGAAGATCTGAAGAACCCTACAAGGACATCCTCAGAGTTGTCAAACAGGTGAAGA
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACCTAGAGTAACTGAAGAACATTTTT
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ACAGGAAGCTTTTATATTACTTGAGTATTTCTGCTTTTCACAGAAAAACATTGGGTTTCTC
TCTGGGTTTGGACATGAAATGTAAGAAAAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAA
ACAAATCTATTAGAGAAACAGCTGGCCCTGCAAAATGTTTACAGAAATGAAATCTTCTCTAC
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAGTGTCT
GGAGTAACAAAATCTCAGTTGGACCATCCTTAACCTGATTGAACCTGTCTAGGAACCTTAC
AGATTGTTCTGCACTTCTCTCTTTTCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC
AGGAATATTGTGGTAAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT
TTGAAACAAGAAACAGAGTGTGTGTAAGGACACCTTCACTGAAGCAAGTCGGAAGTACAA
TGAAAAATAAATTTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT
TTTACTTCTAGGAAGTCTCAAAAGACCATCTTAAATATTATATGTTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCATTGCTTAGCTAACTTTTCAATTCGT
CACTTGGCTTCGATTTTTATATTTTCTATTATATGAAATGTATCTTTGGTGTGTTGATTT
TTCTTTCTTTCTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAGATTTTGCTATAA
TAAAGAAAATCTTGTGACTTTAAAAA

1003167-122701

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400
><subunit 1 of 1, 487 aa, 1 stop
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GPEAPWRDPELLEGTCTPVPQIIVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPPVDADMEFGPPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSPFYEDLKNHYKDILQSCQTSEECELARANSTSEDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCTGCCGCTGGCCCCCTCAGCAACCCCTGCAGATGCGCGCTGAGGCGGGCCACCGCGAC
 TCCGGCTCTGCGCTCGGCTGCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCTGTAGTAGGGCTGTAAATC
 TCAAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTTGATCATTTACGGATTTCG
 AGACAAGTGACCCAGAGATCGATGGGAAGAAAATCAAGATGAACAAACCAATATGTGTTTTTGCACACAAAA
 TTCAGGAGACTTTGGCGGCTGCTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAAATGTGACACGGAGAG
 ACTCAGCCCTTTATCGCTGTGAGGTGCTGCTCGAAATGACCCGCAAGGAAATGTATGAGATTGTGATCGAGTTAA
 CTGTGCAAGTGAAGCCAGTACCCCTGCTGTAGAGTGGCGAAGCTGTACCATAGGCAAGTGGCAACACTGC
 ACTGCCAGGAGAGTGAAGGCGACCCCGGCTCTACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
 CCAGAGCCCAATCCAGATTTCGCAATTTCTTCTCCACTTAAACTCTGAAACAGGCACCTTTGGTGTTCACCTGCT
 TTCAGGAAGGACACTCTGGGCACTACTGCAATGCTTCCAATGACGAGGCTGCCAGGCTGTGAGGAGCAGG
 AGATGGAAGTCTATGACCTGAACATTTGGCGGAATATTGGGGGGTCTGGTGTCTTGTCTGTATGCGCCCTGA
 TCAGTTTGGGCATCTGCTGTGATACAGACGCTGGCTACTTCATCAACAATAAACAGGATGGGAAAGTTTACAAGA
 ACCCAGGGAACCCAGATGGAGTTAACTACATCCGCATGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
 TGATCTTGAACCCCGGTGTGGCTGAGAGCGCACAGAGCGCAGCTGCACATACCTCTGCTAGAAACTCCTGTCAA
 GGCAGCGAGAGCTGTGCTACAGCGAGCTAGACACTCATTCAAGAGCTTTTCGTTTTGGGCCAAAGTTGACCA
 CTACTCTTCTTACTTAAACAGCCAGCTGAATAGAAGATTTCCTCAAGATGAGCCCGGTAAATATAAACCCAA
 GGAAGCAACTGGGTGGCTTCACTAGTTGGGTTCCTAATCTGTTTCTGGCTGATTTCCCGCATGAGATTATAGG
 GTGATCTTAAAGAGTTTGCTCACGTAAACGCCCGTCTGGGCCCTGTGAAGCCAGCATGTTCAACCATGTGTCTT
 CAGCAGCCACGACAGCACCATTGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGAAACCCA
 GAAAGGCTTCTTACACAGCAGCCTTACTTCACTCGGCCACAGACACACCGAGATTCTCTTTAAAGGCTCTGC
 TGATCGGTGTGCAAGTGTCCATGTGTGGAAGAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
 GTAATTTGGTTCTGGAAGAGGATCTTGCCTGAGGAACCTGCTTGTCCACAGGGTGTGAGGATTAAAGGAAA
 ACCTTCTGCTTAGGCTAAGTCTGAATGTGACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTAAAAAATTT
 TACATCTAAATTTTTGTAAAGGATGATTTTGATTATTGAAAAAGAAAATTTCTATTAAACTGTAAATATATTGT
 CATACAATGTAAATAACCTATTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCCAAGCTCATAGTGTAAAT
 TGGAAAAATATCAATAATTAAAGATATTTCACCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTCTCTTTCT
 CACACAAGTTTtagcctttttcaaaagggaactcatactgtctacacatcagaccatagttgctttaggaaaacctt
 TAAAAAATCCAGTTAAGCAATGTGAAATCAGTTTGATCTCTTCAAAAGAAACCTCTCAGGTAGCTTTGAACT
 GCCCTCTCTGAGATGACTAGGACAGCTGTATCCACAGGGCCACCGAAGCCCTCAGATGTACATACACAGATG
 CCAGTCAGCTCCTGGGGTTTGGCGAGGCGCCCCGCTCTAGCTCACTGTGCTCTGCTGCCAGGAGGCCCT
 GCCATCCTTGGGCGCTGGCAGTGGCTGTGTCCAGTGAAGCTTTACTCAAGTGGGCCCTTGCTTCATCAGACAGAG
 TCTCAGGTGGGCACTGAGGGACACTGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTGAACAGAGCTCT
 TTTTGGTTATGGATGGCTCACAAAAATAGGCGCCCAATGCTATTTTTTTTAAAGTTTGTGTTAAATATTGTT
 AAGATTGTCTAAGGCGAAAGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAAGAAAATGGAT
 CCCACTCTTCTCTTTGGCCAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCAATTTCAAAACAACCAATGAT
 GGAGTGGCGGCGAGTCCAGCCTTTTAAAGAACCTGAAGGTGGAGACCCAGGTGAAGAGCCTGGCGGCCCTGGCGGGAAG
 TGAACCGCTGAATCAAAAGCAGTTTCTAATTTTGAATTTTCAATCCGCGGAGAGACTGCTCCCATT
 TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGTGCCCT
 GCCGTGTGAGCTCAGGACTGAAGTCTGTGTAAGCAAGGAGCTGTGAGAAGGAGCACTCCACTGTGTGCTCGGA
 GAATGGCTCTCACTACTCACCCTGTGCTTTCAGCTCCAGTGTCTTGGGTTTTTTTACTCTTGACAGCTTTTTTTT
 AATTGCTACATGAGACTGTTTGACTTTTTTAGTTATGTGAACACTTGGCGGCCGCTGGCAGGAGGCA
 GGAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
 CCTCACTCATTGCCACTTGGTAGAGAGGATGGCTCCCCACCTCAGCGTTGGGGATTCAGGCTCAGGCTCCT
 TCTTGGTTGTATAGTGTATAGGGTAGCCTTATGGCCCTCTCTTATAGCTAAAACTCTACACTAGTGTGCCA
 TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTCAATAGACTAGAC
 CGGAAGAGGAATACTCGTATTTTAAAGATGAATGTGACTCAAGATCAGGAGCCGATACGAGCTGTGATTCT
 GCCTTTGGATGGATGTGCTGTACACAGATGCTACGACTGTACTAACACACCGTAAATTGGCATTTGTTTAAAC
 CTCATTTATAAAGGCTTCAAAAAACCA

FIGURE 14

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
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PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPAVPGKMATLHCQSESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAGGTTCTTCCATCGCTGGAGCAGCGGGGAGACAGCCACATGACACATCCTCGTGGTCCATGCCATGGTG
 ATCTCTGCTGACGCTGGGCCCCCTCGAGCCGACGACAGCGAGTTCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGAGGCCACTGCCCAACCGCTTCTGCTGGGACACATCGAGGAGGCGCTGCTGCTTCTGACTGGCTTGAAGCTG
 CGCATGATCGGTTCTGAGGTGCTCGCGCTGGTGGACCGCGCCCTGCAGGACCTGGAGCCGACGAGCTGCTGCTG
 TTCTGTGATCTCGGTTTGGCATCTCGCTTGCCTGTGCAGCATGAGCAAACTCCTCAGGTTCTGTGGACAGGCGAGTGGCCAC
 GACCCCCAGACTCTGGAGCAGAACTCATGGACAAGAAATTACATGGCCCCACTGGTGGAGGTCCAGCATGAGCGC
 GGGCGCTCCGGAGGCCAGACTTTCACATCTTGTCTCAGACCTCCCTGCCGCCCGCGGAGACAGACACAGGGCA
 CCCAAACCAAGAGCAGCCAGAGCAGCCATAGGCCAGGGCCGAGTTCGGGTGGGGACCCAGCTCCGGGTGCTG
 GGCCCTGAGGACGACCTGGCTGGCATGTTCTCTCCAGATTTCCTCGCTCAGCCCGGACCCCTCGGTGGCAGAGCTCC
 AGTCCCCCGCGTGGCCCTCGCCCTGCGCTGAGCAGGCGCTGGGCCAGGAGCTGGCCCGGCTCGTCCAGGGCAGGCC
 GAGGTGCCGGGCATCAGGTGGCTGTCTGACGGCCCTGCCACCTTGTCTCAGCTCCCCACACGGCGGTGGCCCTG
 GTGATGTCCATGCACCGTAGCCACTTCTCTGGCCTGCCGCTGCTGCTGCCGAGCTCTGCCAGTACCAAGCTGTGTG
 CCACAGGACACCGGCTTCTCTCGCTTCTCTGAAGGTGCTCTCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
 GTGGAGGGCGGGCCCTGCGGGCAGCTCAGGATGCTTGCAGGCGAGGCTCAGCGGGCGCAGGCTCAGTGAT
 GTGCGAGGGGGGCTCTGCGCCCTGGCCGAGGCCCTGGCCTTCCTGAGGACCTGGAGTGGTCAAGCTCCAGCTCCAGCTC
 CGGCGCTGATCGCCACCTTGAGGTTCTGGGAGCAGTGCAGCGTGGAGCGGACCTGATCAGCAAAAGTCTCTCCAG
 GAGTGTGATGAGGTGAGGTCCCCCAGCTGGAGGAGCTGTGATGCAATCTTCTCTGCGACTGCGGATGCTGCC
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 GGGAGGCGGGGTGCGGACGCTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGCTCAGGCCCTCTTAGTGAGTGG
 CTGGAAATGCTGGAGCCCCGAGGTGGTGCAGAGCTGCCCGGACCTGCAGCTCAGGCTGCTCTTCTCCGGAGGAAG
 GGCAAAAGGTGAGGCCAGGTTGCCCTCGTTCCTGCTCCCTACCTCTGACCTCTTACGATCAGCTCCAGCTGGCCCC
 ACATGTCACCAAGTGCATCCGAGTCCGTGTGGCAAGAGCCGGGAAACAGAGGTTGACCCCTGCTCTCTCTGGAC
 TTCTCTTGGGCCCTGCATCATGTTCTCTGCATCTGGCAGGGCGGGACAGCGCACCCCGCAGAAGCGCGGGGAG
 GAGCTGTGCTGCGGGTCCAGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCTTGGCCGAGGCGGAGACCGCG
 AGCCAGGAGCGGGACACAGCCGCTTGCAGCCTCATCCAGGCCGGCTGCCCTGCTGCTGCTCAGTGTGCTGTGGG
 GACGATGAGAGTGTGAGAAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCATGCGGGAGACAGCTGTGTTGGGA
 AGGCGCTGCCGAGACCTTCTCTGAGCTCTACTACAGCGGCCGAGCTGCGGTGCCGTGAGTGTCTTACTGCTCCGAGGAGT
 CTGACAGCGAAGGGGTGCCAGCAGCAGCTGTGCAAGCTGGACGAGTCTATCCACCGCTTATCAGCGCTCTCTT
 GCGGACACAGCGACTCCCGGCGTTGGAGAACCGAGGGCGGATGCCAGCATGGCCCTGCCGGAAGCTGGCGGCTG
 GCGCACCCGCTGCTGCTGCTCAGGCCACTGCCCATGATGCGGGCGCTCTGACGCGCGCACCCACCTCAACTTC
 CAGGAGTTCGCGCAGAGAACCACCTGAGCTGCTTCTGCACTGCTGGGCGCTGCTGGAGCTGCTGAGCCGAC
 TTGTTCCGACGAGCAGCAGGCGGCGCTGTGGGACTGCCCTTCTGTCTTATCGGCTGCTGTAATTACAGG
 AAGTCTCTCCGCCATCTGGCTGCTTCTATCAACAAAGTTTGTGAGTTCATCCATAAGTACATTACTCAATAGCC
 CCAGCAGCCATCTCTTCTGCGAGAAGCAGCGGACCGCTCCAGGACTGCTCTTGCAGAACAGTGAAGTGAAGTGAAGT
 ATGCTGAAATTCCTCCTTGCAGGGCTCAGCCTGCCAGCAGGAGCAGAGGACCGCAGGCGCTGGACGAAGAG
 GCGCAGGAGGAGGACTCAGCGCTCCTTTCGCCCTGGTCAAGCTCTCCCTGTTACCCCTTGAACCGCGGCCGAG
 ATGGCCCCCTACATGAAACGGCTTTCCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTCCCGCGGAGAGCCGAGATCTGAGCTTCTCTGAGCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
 GAGTGTTCGCGCAACTCGCTTTCAGCTGCGCCCTGCGCTCCATGAGAACAGCCAGCAATGACAGCCGCTTTC
 CTGCGGCTGCTTATGTAATGCTGCTGGGAGCAGGACTTGAAGTGTGTGAGCAGGCGCTCCGGAACCTGCTGCTG
 TACGCTCTCTGTGCGCAAGAGCAGCGGCTGTGCTGCTCCACCGGCCCTTCTGCTGGGCATGTACCGGCAGATG
 GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCTGATATGAGGCGCTGATGTGAGCTCTGCGAGCCGA
 CCCCCCTCAAGCCCCGGCCGCTCCGCTCCCGGGGATCTCTGAGGCGAAAGCCAGGAAGCGTGGGCGTTGCTGG
 TCTGTGCGAGGAGTGGGGCGCGAGCCCTGAGGCGAGGCGCCAGGAGCAATATCTCCGAGCAATCTGGGCTGG
 CTCGCGGCGGGCGCTGGCATAGGGGCCGTGACGAGCCCTCAATCACTTCTGCGGCACAGCCCTGCCGCGG
 AGCGCGGATCCCCCGGCGATGGCTGGGCTGTTTGAATGAACGACCTGAAGCTGTCA

4003167.12704

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

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MAHLVEVQHERGASGGQTTFHSLLTASLPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRQLCQYQRCVPQDTGFSSSLFLKVLLQMLQWLDSPG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLRLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASPPACKPVVVVSSLLQEEEEPLA
GGKPGADGGSLEAVRLGPSSGLLVLDWLEMLDPEVVSSCPDLQLRLFLSRRKGKGQAQVPSFR
PYLLTLTFTHQSSWPTLHQCIIRVLLGKSREQRFDPSASLDLFWACIHVPRIWQGRDQRTFPQKR
REELVLRVQGFELISLVELILAEATRSQDGDTAACSLIQARLPLLLSCCGDDSVRKVTE
HLSGCIQQWGDVSLGRRCRDLLLQLYLQRPRLVPVPEVLLHSEGAASSSVCKLDGLIHRFI
TLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLPMIAALLHGRTHLNFQEFRRQNH
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLLNYRKSSRHLAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSDFNSDLVMLKSLLAGLSLPSRDDRTDRGLDEEGEESSAG
SLPLVSVSLTPTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRRPEILSFFSTNLQRL
MSSAECCRNLAFLASLALRSMQNSPSIAAFLPTFMYCLGSQDFEVVQTALRNLPYALLCQE
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,

665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGTCAGCCTCGGCCCCGCGGGCGCCCGCCGCGCACCCGAGGAGATGAGGGCTCCGC
AATGGCACCTTCTGACGCTGCTGCTCTTCTGCTGTGCGCCTTCTCTCGCTGTCTGGTA
CGCGGCACCTACGCGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCTTGGCGC
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTGAGAAAGGAGGCGCTGCGAGACGGAGACGGCAA
TGCACCTGGGGCCGCTAAACAGAGGACCCCGATTGAAGCCGTGGAACGGCTCACACCGG
ACGTGCTGCACCTGCCCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCGCGGTGCGCGTGGGCCAGGGCCGACCCGAGTGTCTGGTGGTGTATGGGATCCC
GAGCGTGGCGCGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTATCGTGGTGTGATCGCCGAGACTGACTCACAG
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCGCCACGGAGATCCATTCTGGGCT
CCTGGAGGTCTCATCTCACCTCCCCCACTTCTACCTGACTTCTCCCGCTCCGAGAGTCTCT
TTGGGGACCCCAAGGAGAGTCAAGGTGAGGACCAACAGAACCTCGATTACTGCTTCCTCT
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA
GCCCCACTACCTGAGCACCATGAAGAACTTTCGACTGCAGCAGCCTTCAGAGGACTGGATGA
TCTTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG
ATTGTAGAGTTCTATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT
TCTGTGGGTGAAAGTCTGCAACCCCGAGAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCAGCACGTGGGCACTCACTCCTCGCTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTTGGAAGCAGGCGCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGTGAGCACGAGCCTGAAGACATACCAGCACTTCACCTTGGAGAAAG
CCTACCTGCGCAGGACTTCTTCTGGGCTTACCCCTGCGCGGGGGGACTTCTACCGCTTC
CGCTTCTTCAAACCTCTAAGACTGGAGCGGTTCTTCTCCGAGTGGGAACATCGAGCACCC
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAAACCTCAGTCAGACA
AGGAGGCTTGCAGGAGGGCCGACCCGCCACCTCCGGTACCTCGGAGCCCCGAGCGCTAC
TCCAGATCGGCTCCTTCTACAAGGAGTGGCAGAGGAGAGGTGGACCCAGCCTTCGGCCC
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCTGAAAAAGGCCGAGTAAAGCTGCGGGCTTCTGAGGGTACCTGTGGCCAGCCCTGAA
GCCCCACATTTCTGGGGTGTCTGCTACTGCGGTCCCCGAGGGCCAGATACGGCCCCGCCAA
AGGGTTCTGCCTGGCGTCGGGCTTGGGCGGGCTGCGGTCGCCCGCTGGCCCGGAGGCCCTA
GGAGCTGGTGTGCCCCCGCCCGCGGGCCGCGAGGAGGCGAGGCGGCCCCCACTGTGCC
TGAGGCCCGGAACCGTTGCGACCCGGCCTGCCCGAGTCAGGCGGTTTTAGAAGAGCTTTTAC
TTGGGCGCCCGCGCTCTCTGGGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT
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AAAAAAAAAAAAAAAA

FIGURE 18

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307
><subunit 1 of 1, 548 aa, 1 stop
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KESSLQPAVRVGGQRTGVSVMGIPSVRREVHSHYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYPDFSRLRESFGDPKERVVRWRTKQNL
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFGHVGH
SSLAGKIQLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLFPDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515